

SEQUENCE LISTING

<110> O'Donohue, Michael R.
Hanke, Paul D.

<120> Methods for Producing L-Amino Acids

<130> 1533.1010002

<140>

<141>

<150> 60/150,017

<151> 1999-08-20

<150> 60/145,217

<151> 1999-07-23

<160> 4

<170> PatentIn Ver. 2.1

<210> 1

<211> 1623

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1620)

<400> 1

atg	gcg	gac	att	tcg	acc	acc	cag	gct	tgg	caa	gac	ctg	acc	gat	cat	48
Met	Ala	Asp	Ile	Ser	Thr	Thr	Gln	Ala	Trp	Gln	Asp	Leu	Thr	Asp	His	
1				5					10					15		

tac	tca	aac	ttc	cag	gca	acc	act	ctg	cgt	gaa	ctt	ttc	aag	gaa	gaa	96
Tyr	Ser	Asn	Phe	Gln	Ala	Thr	Thr	Leu	Arg	Glu	Leu	Phe	Lys	Glu	Glu	
		20						25					30			

aac	cgc	gcc	gag	aag	tac	acc	ttc	tcc	gcg	gct	ggc	ctc	cac	gtc	gac	144
Asn	Arg	Ala	Glu	Lys	Tyr	Thr	Phe	Ser	Ala	Ala	Gly	Leu	His	Val	Asp	
		35					40					45				

ctg	tcg	aag	aat	ctg	ctt	gac	gac	gcc	acc	ctc	acc	aag	ctc	ctt	gca	192
Leu	Ser	Lys	Asn	Leu	Leu	Asp	Asp	Ala	Thr	Leu	Thr	Lys	Leu	Leu	Ala	
	50					55				60						

ctg	acc	gaa	gaa	tct	ggc	ctt	cgc	gaa	cgc	att	gac	gcg	atg	ttt	gcc	240
Leu	Thr	Glu	Glu	Ser	Gly	Leu	Arg	Glu	Arg	Ile	Asp	Ala	Met	Phe	Ala	
	65				70					75					80	

ggt	gaa	cac	ctc	aac	aac	acc	gaa	gac	cgc	gct	gtc	ctc	cac	acc	gcg	288
Gly	Glu	His	Leu	Asn	Asn	Thr	Glu	Asp	Arg	Ala	Val	Leu	His	Thr	Ala	
			85						90					95		

ctg	cgc	ctt	cct	ccc	gaa	gct	gat	ctg	tca	gta	gat	ggc	caa	gat	gtt	336
Leu	Arg	Leu	Pro	Pro	Glu	Ala	Asp	Leu	Ser	Val	Asp	Gly	Gln	Asp	Val	
			100					105					110			

gct	gct	gat	gtc	cac	gaa	gtt	ttg	gga	cgc	atg	cgt	gac	ttc	gct	act	384
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

Ala	Ala	Asp	Val	His	Glu	Val	Leu	Gly	Arg	Met	Arg	Asp	Phe	Ala	Thr		
		115					120					125					
gcg	ctg	cgc	tca	ggc	aac	tgg	ttg	gga	cac	acc	ggc	cac	acg	atc	aag	432	
Ala	Leu	Arg	Ser	Gly	Asn	Trp	Leu	Gly	His	Thr	Gly	His	Thr	Ile	Lys		
	130					135					140						
aag	atc	gtc	aac	att	ggc	atc	ggc	ggc	tct	gac	ctc	gga	cca	gcc	atg	480	
Lys	Ile	Val	Asn	Ile	Gly	Ile	Gly	Gly	Ser	Asp	Leu	Gly	Pro	Ala	Met		
145					150					155					160		
gct	acg	aag	gct	ctg	cgt	gca	tac	gcg	acc	gct	ggc	atc	tca	gca	gaa	528	
Ala	Thr	Lys	Ala	Leu	Arg	Ala	Tyr	Ala	Thr	Ala	Gly	Ile	Ser	Ala	Glu		
				165					170					175			
ttc	gtc	tcc	aac	gtc	gac	cca	gca	gac	ctc	gtt	tct	gtg	ttg	gaa	gac	576	
Phe	Val	Ser	Asn	Val	Asp	Pro	Ala	Asp	Leu	Val	Ser	Val	Leu	Glu	Asp		
			180					185					190				
ctc	gat	gca	gaa	tcc	aca	ttg	ttc	gtg	atc	gct	tcg	aaa	act	ttt	acc	624	
Leu	Asp	Ala	Glu	Ser	Thr	Leu	Phe	Val	Ile	Ala	Ser	Lys	Thr	Phe	Thr		
		195					200					205					
acc	cag	gag	acg	ctg	tct	aac	gct	cgt	gca	gct	cgt	gct	tggt	ctg	gta	672	
Thr	Gln	Glu	Thr	Leu	Ser	Asn	Ala	Arg	Ala	Ala	Arg	Ala	Trp	Leu	Val		
	210					215					220						
gag	aag	ctc	ggc	gaa	gag	gct	gtc	gcg	aag	cat	ttc	gtc	gca	gtg	tcc	720	
Glu	Lys	Leu	Gly	Glu	Glu	Ala	Val	Ala	Lys	His	Phe	Val	Ala	Val	Ser		
225				230						235					240		
acc	aat	gct	gaa	aag	gtc	gca	gag	ttc	ggc	atc	gac	acg	gac	aac	atg	768	
Thr	Asn	Ala	Glu	Lys	Val	Ala	Glu	Phe	Gly	Ile	Asp	Thr	Asp	Asn	Met		
				245					250					255			
ttc	ggc	ttc	tgg	gac	tgg	gtc	gga	ggc	cgt	tac	tcc	gtg	gac	tcc	gca	816	
Phe	Gly	Phe	Trp	Asp	Trp	Val	Gly	Gly	Arg	Tyr	Ser	Val	Asp	Ser	Ala		
			260					265					270				
gtt	ggc	ctt	tcc	ctc	atg	gca	gtg	atc	ggc	cct	cgc	gac	ttc	atg	cgt	864	
Val	Gly	Leu	Ser	Leu	Met	Ala	Val	Ile	Gly	Pro	Arg	Asp	Phe	Met	Arg		
		275					280					285					
ttc	ctc	ggc	gga	ttc	cac	gcg	atg	gat	gaa	cac	ttc	cgc	acc	acc	aag	912	
Phe	Leu	Gly	Gly	Phe	His	Ala	Met	Asp	Glu	His	Phe	Arg	Thr	Thr	Lys		
	290					295					300						
ttc	gaa	gag	aac	gtt	cca	atc	ttg	atg	gct	ctg	ctc	ggc	gtc	tgg	tac	960	
Phe	Glu	Glu	Asn	Val	Pro	Ile	Leu	Met	Ala	Leu	Gly	Val	Trp	Tyr			
305					310					315				320			
tcc	gat	ttc	tat	ggc	gca	gaa	acc	cac	gct	gtc	cta	cct	tat	tcc	gag	1008	
Ser	Asp	Phe	Tyr	Gly	Ala	Glu	Thr	His	Ala	Val	Leu	Pro	Tyr	Ser	Glu		
				325					330					335			
gat	ctc	agc	cgt	ttt	gct	gct	tac	ctc	cag	cag	ctg	acc	atg	gaa	tca	1056	
Asp	Leu	Ser	Arg	Phe	Ala	Ala	Tyr	Leu	Gln	Gln	Leu	Thr	Met	Glu	Ser		
			340					345					350				
aac	ggc	aag	tca	gtc	cac	cgc	gac	ggc	tcc	cct	gtt	tcc	act	ggc	act	1104	
Asn	Gly	Lys	Ser	Val	His	Arg	Asp	Gly	Ser	Pro	Val	Ser	Thr	Gly	Thr		
		355					360					365					

ggc gaa att tac tgg ggt gag cct ggc aca aat ggc cag cac gct ttc 1152
 Gly Glu Ile Tyr Trp Gly Glu Pro Gly Thr Asn Gly Gln His Ala Phe
 370 375 380

ttc cag ctg atc cac cag ggc act cgc ctt gtt cca gct gat ttc att 1200
 Phe Gln Leu Ile His Gln Gly Thr Arg Leu Val Pro Ala Asp Phe Ile
 385 390 395 400

ggt ttc gct cgt cca aag cag gat ctt cct gcc ggt gag cgc acc atg 1248
 Gly Phe Ala Arg Pro Lys Gln Asp Leu Pro Ala Gly Glu Arg Thr Met
 405 410 415

cat gac ctt ttg atg agc aac ttc ttc gca cag acc aag gtt ttg gct 1296
 His Asp Leu Leu Met Ser Asn Phe Phe Ala Gln Thr Lys Val Leu Ala
 420 425 430

ttc ggt aag aac gct gaa gag atc gct gcg gaa ggt gtc gca cct gag 1344
 Phe Gly Lys Asn Ala Glu Glu Ile Ala Ala Glu Gly Val Ala Pro Glu
 435 440 445

ctg gtc aac cac aag gtc atg cca ggt aat cgc cca acc acc acc att 1392
 Leu Val Asn His Lys Val Met Pro Gly Asn Arg Pro Thr Thr Thr Ile
 450 455 460

ttg gcg gag gaa ctt acc cct tct att ctc ggt gcg ttg atc gct ttg 1440
 Leu Ala Glu Glu Leu Thr Pro Ser Ile Leu Gly Ala Leu Ile Ala Leu
 465 470 475 480

tac gaa cac atc gtg atg gtt cag ggc gtg att tgg gac atc aac tcc 1488
 Tyr Glu His Ile Val Met Val Gln Gly Val Ile Trp Asp Ile Asn Ser
 485 490 495

ttc gac caa tgg ggt gtt gaa ctg ggc aaa cag cag gca aat gac ctc 1536
 Phe Asp Gln Trp Gly Val Glu Leu Gly Lys Gln Gln Ala Asn Asp Leu
 500 505 510

gct ccg gct gtc tct ggt gaa gag gat gtt gac tcg gga gat tct tcc 1584
 Ala Pro Ala Val Ser Gly Glu Glu Asp Val Asp Ser Gly Asp Ser Ser
 515 520 525

act gat tca ctg att aag tgg tac cgc gca aat agg tag 1623
 Thr Asp Ser Leu Ile Lys Trp Tyr Arg Ala Asn Arg
 530 535 540

<210> 2

<211> 540

<212> PRT

<213> Corynebacterium glutamicum

<400> 2

Met Ala Asp Ile Ser Thr Thr Gln Ala Trp Gln Asp Leu Thr Asp His
 1 5 10 15

Tyr Ser Asn Phe Gln Ala Thr Thr Leu Arg Glu Leu Phe Lys Glu Glu
 20 25 30

Asn Arg Ala Glu Lys Tyr Thr Phe Ser Ala Ala Gly Leu His Val Asp
 35 40 45

Leu Ser Lys Asn Leu Leu Asp Asp Ala Thr Leu Thr Lys Leu Leu Ala
 50 55 60

Leu Thr Glu Glu Ser Gly Leu Arg Glu Arg Ile Asp Ala Met Phe Ala
 65 70 75 80
 Gly Glu His Leu Asn Asn Thr Glu Asp Arg Ala Val Leu His Thr Ala
 85 90 95
 Leu Arg Leu Pro Pro Glu Ala Asp Leu Ser Val Asp Gly Gln Asp Val
 100 105 110
 Ala Ala Asp Val His Glu Val Leu Gly Arg Met Arg Asp Phe Ala Thr
 115 120 125
 Ala Leu Arg Ser Gly Asn Trp Leu Gly His Thr Gly His Thr Ile Lys
 130 135 140
 Lys Ile Val Asn Ile Gly Ile Gly Gly Ser Asp Leu Gly Pro Ala Met
 145 150 155 160
 Ala Thr Lys Ala Leu Arg Ala Tyr Ala Thr Ala Gly Ile Ser Ala Glu
 165 170 175
 Phe Val Ser Asn Val Asp Pro Ala Asp Leu Val Ser Val Leu Glu Asp
 180 185 190
 Leu Asp Ala Glu Ser Thr Leu Phe Val Ile Ala Ser Lys Thr Phe Thr
 195 200 205
 Thr Gln Glu Thr Leu Ser Asn Ala Arg Ala Ala Arg Ala Trp Leu Val
 210 215 220
 Glu Lys Leu Gly Glu Glu Ala Val Ala Lys His Phe Val Ala Val Ser
 225 230 235 240
 Thr Asn Ala Glu Lys Val Ala Glu Phe Gly Ile Asp Thr Asp Asn Met
 245 250 255
 Phe Gly Phe Trp Asp Trp Val Gly Gly Arg Tyr Ser Val Asp Ser Ala
 260 265 270
 Val Gly Leu Ser Leu Met Ala Val Ile Gly Pro Arg Asp Phe Met Arg
 275 280 285
 Phe Leu Gly Gly Phe His Ala Met Asp Glu His Phe Arg Thr Thr Lys
 290 295 300
 Phe Glu Glu Asn Val Pro Ile Leu Met Ala Leu Leu Gly Val Trp Tyr
 305 310 315 320
 Ser Asp Phe Tyr Gly Ala Glu Thr His Ala Val Leu Pro Tyr Ser Glu
 325 330 335
 Asp Leu Ser Arg Phe Ala Ala Tyr Leu Gln Gln Leu Thr Met Glu Ser
 340 345 350
 Asn Gly Lys Ser Val His Arg Asp Gly Ser Pro Val Ser Thr Gly Thr
 355 360 365
 Gly Glu Ile Tyr Trp Gly Glu Pro Gly Thr Asn Gly Gln His Ala Phe
 370 375 380
 Phe Gln Leu Ile His Gln Gly Thr Arg Leu Val Pro Ala Asp Phe Ile
 385 390 395 400

Gly	Phe	Ala	Arg	Pro	Lys	Gln	Asp	Leu	Pro	Ala	Gly	Glu	Arg	Thr	Met
				405					410					415	
His	Asp	Leu	Leu	Met	Ser	Asn	Phe	Phe	Ala	Gln	Thr	Lys	Val	Leu	Ala
			420					425					430		
Phe	Gly	Lys	Asn	Ala	Glu	Glu	Ile	Ala	Ala	Glu	Gly	Val	Ala	Pro	Glu
		435					440					445			
Leu	Val	Asn	His	Lys	Val	Met	Pro	Gly	Asn	Arg	Pro	Thr	Thr	Thr	Ile
	450					455					460				
Leu	Ala	Glu	Glu	Leu	Thr	Pro	Ser	Ile	Leu	Gly	Ala	Leu	Ile	Ala	Leu
465					470					475					480
Tyr	Glu	His	Ile	Val	Met	Val	Gln	Gly	Val	Ile	Trp	Asp	Ile	Asn	Ser
				485					490					495	
Phe	Asp	Gln	Trp	Gly	Val	Glu	Leu	Gly	Lys	Gln	Gln	Ala	Asn	Asp	Leu
			500					505					510		
Ala	Pro	Ala	Val	Ser	Gly	Glu	Glu	Asp	Val	Asp	Ser	Gly	Asp	Ser	Ser
		515					520					525			
Thr	Asp	Ser	Leu	Ile	Lys	Trp	Tyr	Arg	Ala	Asn	Arg				
	530					535					540				

<210> 3
 <211> 25
 <212> DNA
 <213> Corynebacterium glutamicum

<400> 3
 gctgatgtcc acgaagcttt gggac

25

<210> 4
 <211> 25
 <212> DNA
 <213> Corynebacterium glutamicum

<400> 4
 gctgagaacc ttggaataag gtagg

25